

Thu, Mar 15 11:53:15 2001

us

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Db 310 ATGCTGTACTTTAAAGTTGGTAATGAACACACCTAAAGTATATAAATCACAACCTATAACAGAT 251
QY 481 gtttaagcctacagatgtaggagttcttagatgaacacaaagggtaaagataaacaatttaaca 540
Db 250 GTTAAGCCTACAGATGTAGGAGTTCTAGATGAACAAAAAGGTAAAGATAAACCAATTAAACA 191
QY 541 ttaattacttctgtagattacaaatgaagaacagagcggtttgggaaaaacgtaaaatcttt 600
Db 190 TTAATTACTTGTGATGATTACATGAAAGACAGAGCGTTTGGGAAAAACGTAAANCTTTT 131
QY 601 gtagctacagaagtcataataa 621
Db 130 GTAGCTACAGAAGTCARATAA 110
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Query Match      100.0%; Score 621; DB 11; Length 3733;
Best local similarity 100.0%; Pred. No. 1.2e-106;
Matches 621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 atgaaaataaggcaaaatcgattaatgcacatcgcgtggtgtggtactcttcctagtgcca 60
DB      730 atgaaaaaaatggcaaaatcgattaatgcacatcgcgtggtgtggtactcttcctagtgcca 671

QY      61 gcaattgtgttgcaaaacccacatcgcataaattcttcacgcatacaagatacaagatgcaa 120
DB      670 gcataattgttttctaaaccacatcgcataaattcttcacgcatacaagatacaagatgcaa 611

QY      121 aagattgaacaaatcgataaaatgtaaaagaacgcgcgcgttaaagataaaaaagcagcaaa 180
DB      610 aagattgaacaaatgatataaaatgtaaaagaacgcgcgcgttaaagataaaaaagcagcaaa 551

QY      181 gctaaacctcaaatctcgaaagataaaatcgaaagtcgcgcgcgtcattattgaaattccagat 240
DB      550 gctaaacctcnaattccgaaagataaaatcgaaagtcgcgcgcgtcattattgaaattccagat 491

QY      241 gctgatattaagaagaccgttatctcaggaccagcaaacctcgacaatttaataagagt 300
DB      490 gctgatatttaagaagaccagtattctcaggaccagcaaacctcgacaatttaataagagt 431

QY      301 gtaagctttgcagaagaaaatgaaatcactcagatgatacaaaatattttcaattgcaggacac 360
DB      430 gtaagctttgcagaagaaaatgaaatcactcagatgatacaaaatattttcaattgcaggacac 371

QY      361 acttcaattgacgctccgaactatcaaatcttcaaaactttaaagcagcccaaaaaggtagt 420
DB      370 acttcaattgacgctccgaactatcaaatcttcaaaactttaaagcagcccaaaaaggtagt 311

QY      421 atgctgactttcaagagttggcaatgaaacacgcataaataatgacaaagataaagaagat 480
DB      311 atgctgactttcaagagttggcaatgaaacacgcataaataatgacaaagataaagaagat 480

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RESULT 2
US-08-781-986A-538/c
: Sequence 538, Application US/08781986A